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Section 16-5. Metabolism of Hexoses Other Than Glucose 477

derived from fruits and from the hydrolysis of sucrose (table sugar); galactose, obtained from the hydrolysis of lactose (milk sugar); and mannose, obtained from the digestion of polysaccharides and glycoproteins. After digestion, the monosaccharides enter the bloodstream, which carries them to various tissues. The metabolism of fructose, galactose, and mannose proceeds by their conversion to glycolytic intermediates, from which point they are broken down identically to glucose.

A. Fructose

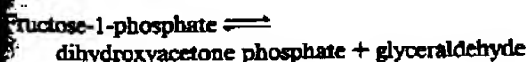
Fructose is a major fuel source in diets that contain large amounts of sucrose (a disaccharide of fructose and glucose). There are two pathways for the metabolism of fructose; one occurs in muscle and the other occurs in liver. This dichotomy results from the different enzymes present in these various tissues.

Fructose metabolism in muscle differs little from that of glucose. Hexokinase (Section 16-2A), which converts glucose to G6P on entry into muscle cells, also phosphorylates fructose, yielding F6P (Fig. 16-34, left). The entry of fructose into glycolysis therefore involves only one reaction.

Liver contains little hexokinase; rather it contains glucokinase, which phosphorylates only glucose (Section 16-2A). Fructose metabolism in liver must therefore differ from that in muscle. In fact, liver converts fructose to glycolytic intermediates through a pathway that involves six enzymes (Fig. 16-34, right):

Fructokinase catalyzes the phosphorylation of fructose by ATP at C1 to form fructose-1-phosphate. Neither hexokinase nor phosphofructokinase can phosphorylate fructose-1-phosphate at C6 to form the glycolytic intermediate fructose-1,6-bisphosphate.

Class I aldolase (Section 16-2D) has several isoenzymic forms. Muscle contains Type A aldolase, which is specific for fructose-1,6-bisphosphate. Liver, however, contains Type B aldolase, which also utilizes fructose-1-phosphate as a substrate (Type B aldolase is sometimes called fructose-1-phosphate aldolase). In liver, fructose-1-phosphate therefore undergoes an aldol cleavage (Section 16-2D):



The glyceraldehyde thus formed is converted to glyceraldehyde-3-phosphate by Reaction 3, or to dihydroxyacetone phosphate by a combination of Reactions 4 to 6 (Fig. 16-34).

Direct phosphorylation of glyceraldehyde by ATP through the action of glyceraldehyde kinase forms the glycolytic intermediate glyceraldehyde-3-phosphate.

Alternatively, glyceraldehyde is converted to the glycolytic intermediate dihydroxyacetone phosphate by

reduction to glycerol by NAD⁺ as catalyzed by alcohol dehydrogenase (Reaction 4), phosphorylation to glycerol-3-phosphate by ATP through the action of glycerol kinase (Reaction 5), and reoxidation by NADH to dihydroxyacetone phosphate as mediated by glycerol phosphate dehydrogenase (Reaction 6).

As this complex series of reactions suggests, the liver has an enormous repertory of enzymes. This is because the liver is involved in the breakdown of a great variety of metabolites. Efficiency in metabolic processing dictates that many of these substances be converted to glycolytic intermediates. The liver, in fact, contains many of the enzymes necessary to do so.

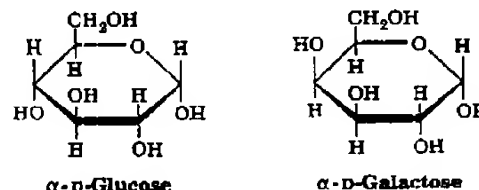
Excessive Fructose Depletes Liver P_i

At one time, fructose was thought to have advantages over glucose for intravenous feeding. The liver, however, encounters metabolic problems when the blood concentration of this sugar is too high (higher than can be attained by simply eating fructose-containing foods). When the fructose concentration is high, fructose-1-phosphate may be produced faster than Type B aldolase can cleave it. Intravenous feeding of large amounts of fructose may therefore result in high enough fructose-1-phosphate accumulation to severely deplete the liver's store of P_i. Under these conditions, [ATP] drops, thereby activating glycolysis and lactate production. The lactate concentration in the blood under such conditions can reach life-threatening levels.

Fructose intolerance, a genetic disease in which ingestion of fructose causes the same fructose-1-phosphate accumulation as with its intravenous feeding, results from a deficiency of Type B aldolase. This condition appears to be self-limiting: Individuals with fructose intolerance rapidly develop a strong distaste for anything sweet.

B. Galactose

Galactose comprises half of the milk sugar lactose, and is thus a major fuel constituent of dairy products. Galactose and glucose are epimers that differ only in their configuration about C4.



The enzymes of glycolysis are specific; they do not recognize the galactose configuration. An epimerization reaction must therefore be carried out before galactose enters the glycolytic pathway. This reaction takes place after the conversion of galactose to its uridine diphosphate derivative.

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The role of UDP-sugars and other nucleotidyl-sugars is discussed in more detail in Sections 17-2 and 21-3. The entire pathway converting galactose to a glycolytic intermediate involves four reactions (Fig. 16-35):

1. Galactose is phosphorylated at C1 by ATP in a reaction catalyzed by galactokinase.
2. Galactose-1-phosphate uridylyl transferase transfers the uridylyl group of UDP-glucose to galactose-1-phosphate to yield glucose-1-phosphate (G1P) and UDP-galactose by the reversible cleavage of UDP-glucose's pyrophosphoryl bond.
3. UDP-galactose-4-epimerase converts UDP-galactose back to UDP-glucose. This enzyme has an associated NAD^+ , which suggests that the reaction involves the

sequential oxidation and reduction of the hexose C atom:

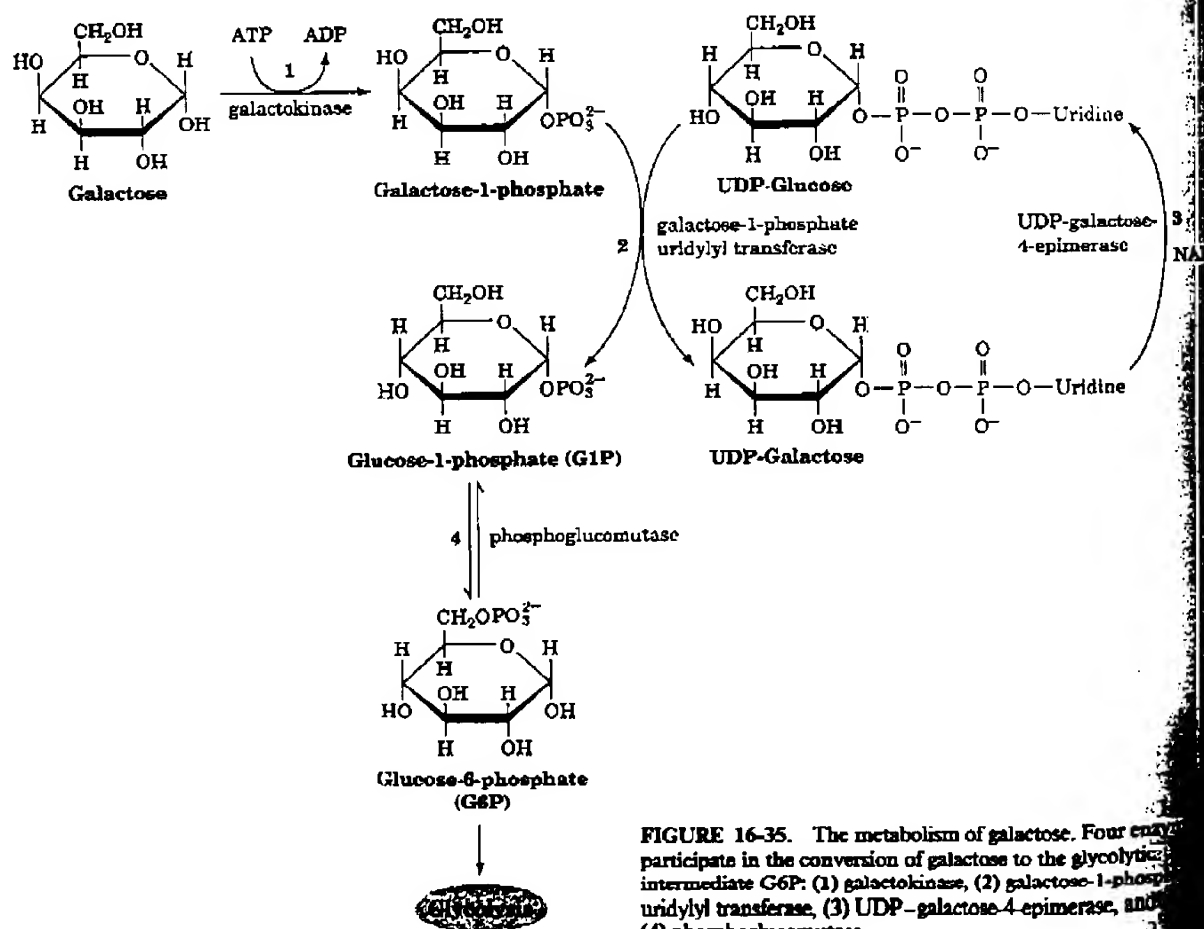
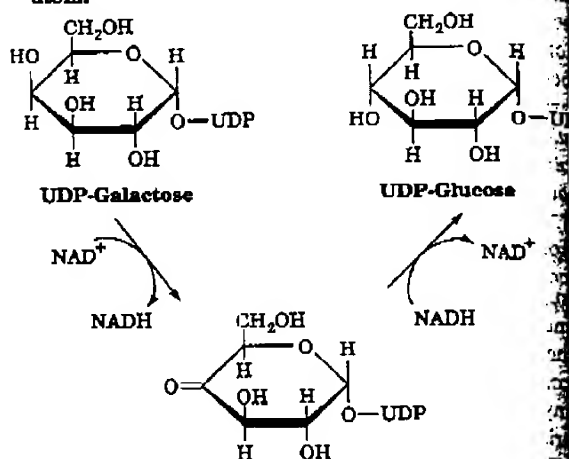


FIGURE 16-35. The metabolism of galactose. Four enzymes participate in the conversion of galactose to the glycolytic intermediate G6P: (1) galactokinase, (2) galactose-1-phosphate uridylyl transferase, (3) UDP-galactose-4-epimerase, and (4) phosphoglucomutase.

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| | |
|--|--|
| Official Name | |
| UTP--hexose-1-phosphate uridylyltransferase. | |
| Alternative Name(s) | |
| Galactose-1-phosphate uridylyltransferase. | |
| Reaction catalysed | |
| UTP + alpha-D-galactose 1-phosphate <=> diphosphate + UDP-galactose | |
| Comments | |
| <ul style="list-style-type: none"> Alpha-D-glucose 1-phosphate can also act as acceptor, more slowly. | |
| Human Genetic Disease(s) | |
| Galactosemia | MIM:230400 |
| Cross-references | |
| Biochemical Pathways; map number(s) | B4 |
| PROSITE | PDOC00108 |
| BRENDA | 2.7.7.10 |
| EMP/PUMA | 2.7.7.10 |
| WIT | 2.7.7.10 |
| KYOTO UNIVERSITY LIGAND CHEMICAL DATABASE | 2.7.7.10 |
| IUBMB Enzyme Nomenclature | 2.7.7.10 |
| MEDLINE | Find literature relating to 2.7.7.10 |
| Swiss-Prot | F40908, GAL7_CRYNE; P09148, GAL7_ECOLI; P31764, GAL7_HAEIN; P07902, GAL7_HUMAN; P09530, GAL7_KLULA; Q03249, GAL7_MOUSE; P43424, GAL7_RAT; P22714, GAL7_SALTY; Q9H005, GAL7_SCHPO; P13212, GAL7_STRLI; Q33836, GAL7_THEMA; P09431, GAL7_YEAST; Q9KDV2, GALT_BACHD; P39575, GALT_BACSU; P45981, GALT_BUTFI; Q97E24, GALT_CLOAB; Q8XKP3, GALT_CLOPE; Q8RHC9, GALT_FUSNN; Q84904, GALT_LACCA; Q00051, GALT_LACHE; Q9CE63, GALT_LACLA; Q9S653, GALT_LACLC; Q93MM1, GALT_LACSK; Q9RGR9, GALT_STACA; P96994, GALT_STRMU; Q8VS92, GALT_STRSL; Q9ZB09, GALT_STRTR; Q8R8R6, GALT_THETN; Q97E15, GAT1_STRFN; Q97N27, GAT2_STRFN; |

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General information about the entry

Entry name **GAL7_ECOLI**
Primary accession number **P09148**
Secondary accession number **P78270**
Entered in Swiss-Prot in **Release 10, March 1989**
Sequence was last modified in **Release 35, November 1997**
Annotations were last modified in **Release 41, February 2003**
Name and origin of the protein
Protein name **Galactose-1-phosphate uridylyltransferase**
Synonym **EC 2.7.7.10**
Gene name **GALT or GALB or B0758**
From **Escherichia coli [TaxID: 562]**
Taxonomy **Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales; Enterobacteriaceae; Escherichia.**

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Comments

- **CATALYTIC ACTIVITY:** UTP + alpha-D-galactose 1-phosphate = diphosphate + UDP-galactose.
- **PATHWAY:** Galactose metabolism; second step.
- **SUBUNIT:** Homodimer.
- **SIMILARITY:** BELONGS TO THE GALACTOSE-1-PHOSPHATE URIDYLTRANSFERASE FAMILY 1.

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Cross-references

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AE000178; AAC73845.1; -. [[EMBL](#)] / [[GenBank](#)] / [[DDBJ](#)] [[CoDingSequence](#)]
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PIR S00722; XNECUD.

PDB 1GUP; 12-NOV-97. [[ExPASy](#)] / [[RCSB](#)]
1GUQ; 12-NOV-97. [[ExPASy](#)] / [[RCSB](#)]
1HXP; 08-NOV-96. [[ExPASy](#)] / [[RCSB](#)]
1HXQ; 22-OCT-97. [[ExPASy](#)] / [[RCSB](#)]
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EcoGene EG10366; galT.

EcoCyc EG10366; galT.

CMR P09148; B0758.
[IPR001937](#); GalP_UDPtransf1.
[IPR005851](#); GalP_Utransf_1.
[IPR005850](#); GalP_Utransf_C.
[IPR005849](#); GalP_Utransf_N.
[Graphical view of domain structure.](#)

Pfam PF01087; GalP_UDP_transf; 1.
PF02744; GalP_UDP_tr_C; 1.
[PD005051](#); GalP_UDPtransf1; 1.
[\[Domain structure / List of seq. sharing at least 1 domain\].](#)

ProDom

TIGRFAMs TIGR00209; galT_1; 1.

PROSITE PS00117; GAL_P_UDP_TRANSF_1; 1.

BLOCKS P09148.

ProtoNet P09148.

ProtoMap P09148.

PRESAGE P09148.

DIP P09148.

ModBase P09148.

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Keywords

Transferase; Nucleotidyltransferase; Galactose metabolism; 3D-structure; Complete proteome.

Features



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Sequence information

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| ELSVAALTEI | VKTWQEQTAE | LGKTPPWQV | FENKGAAMGC | SNPHFHGQIW | ANSFLPNEAE |
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| | |
|---|---|
| Official Name | |
| Galactokinase. | |
| Alternative Name(s) | |
| None. | |
| Reaction catalysed | |
| ATP + D-galactose <=> ADP + D-galactose 1-phosphate | |
| Comments | |
| <ul style="list-style-type: none"> D-galactosamine can also act as acceptor. | |
| Human Genetic Disease(s) | |
| Galactokinase deficiency | MIM:230200 |
| Cross-references | |
| Biochemical Pathways; map number(s) | B4 |
| PROSITE | PDOC00099, PDOC00545 |
| BRENDA | 2.7.1.6 |
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| KYOTO UNIVERSITY LIGAND CHEMICAL DATABASE | 2.7.1.6 |
| IUBMB Enzyme Nomenclature | 2.7.1.6 |
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| Swiss-Prot | P94169, GAL1_ACTPL; Q9SEE5, GAL1_ARATH; Q9KOV4, GAL1_BACHD; P39574, GAL1_BACSU; P56091, GAL1_CANAL; P56599, GAL1_CANMA; Q42821, GAL1_CANPA; Q97E26, GAL1_CLOAB; Q8XKP9, GAL1_CLOPE; P06976, GAL1_ECOLI; Q8RHD0, GAL1_FUSNN; P31767, GAL1_HAEIN; E51570, GAL1_HUMAN; P09608, GAL1_KLULA; Q84902, GAL1_LACCA; Q00052, GAL1_LACHE; Q9R7D7, GAL1_LACLA; Q9S682, GAL1_LACLC; Q9RON0, GAL1_MOUSE; F96910, GAL1_MYCTU; P57892, GAL1_PASMU; Q9HHB6, GAL1_PYRFU; O58107, GAL1_PYRHO; Q8Z8B0, GAL1_SALT1; F22713, GAL1_SALTY; Q9HDU2, GAL1_SCHPO; Q9RGS1, GAL1_STACA; Q9K358, GAL1_STRCO; F13227, GAL1_STRLI; P96923, GAL1_STRMU; Q97NZ6, GAL1_STRPN; Q92B10, GAL1_STRTR; P56838, GAL1_THEMA; Q85253, GAL1_THENE; Q8R8R7, GAL1_THETN; Q83433, GAL1_TREPA; Q9KRP1, GAL1_VIBCH; P04385, GAL1_YEAST; Q8ZGY3, GAL1_YERPE; |

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General information about the entry

Entry name **GAL1_ECOLI**
 Primary accession number **P06976**
 Secondary accession numbers **None**
 Entered in Swiss-Prot in **Release 07, April 1988**
 Sequence was last modified in **Release 10, March 1989**
 Annotations were last modified in **Release 41, February 2003**
 Name and origin of the protein
 Protein name **Galactokinase**
 Synonyms **EC 2.7.1.6
 Galactose kinase**
 Gene name **GALK or GALA or B0757 or Z0927 or ECS0785**
 From **Escherichia coli [TaxID: 562]
 Escherichia coli O157:H7 [TaxID: 83334]**
 Taxonomy **Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales; Enterobacteriaceae; Escherichia**

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- [4] SEQUENCE FROM NUCLEIC ACID.
 STRAIN=O157:H7 / EDL933 / ATCC 700927;
 MEDLINE=21074935; PubMed=11206551; [NCBI, ExPASy, EBI, Israel, Japan]
 Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D., Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A., Postel G.,
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 STRAIN=O157:H7 / RIMD 0509952;
 MEDLINE=21156231; PubMed=11258796; [NCBI, ExPASy, EBI, Israel, Japan]
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MEDLINE=95055764; PubMed=7966338; [NCBI, ExPASy, EBI, Israel, Japan]

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"Dependence of lactose metabolism upon mutarotase encoded in the gal operon in *Escherichia coli*.";
J. Mol. Biol. 244:269-278(1994).

[7] SEQUENCE OF 1-19.

MEDLINE=78043686; PubMed=200486; [NCBI, ExPASy, EBI, Israel, Japan]

Schlesinger D.H., Schell M.A., Wilson D.B.;

"The NH2-terminal sequences of galactokinase from *Escherichia coli* and *Saccharomyces cerevisiae*.";
FEBS Lett. 83:45-47(1977).

Comments

- **CATALYTIC ACTIVITY:** ATP + D-galactose = ADP + D-galactose 1-phosphate.
- **PATHWAY:** Galactose metabolism; first step.
- **SUBCELLULAR LOCATION:** Cytoplasmic (*Potential*).
- **SIMILARITY:** BELONGS TO THE GHMP KINASE FAMILY. GALK SUBFAMILY.

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Cross-references

| | |
|--------------|--|
| EMBL | X02306; CAA26172.1; -. [EMBL / GenBank / DDBJ] [CoDingSequence] AE000178; AAC73844.1; -. [EMBL / GenBank / DDBJ] [CoDingSequence] D90714; BAA35419.1; -. [EMBL / GenBank / DDBJ] [CoDingSequence] AE005253; AAG55086.1; -. [EMBL / GenBank / DDBJ] [CoDingSequence] AP002555; BAB34208.1; -. [EMBL / GenBank / DDBJ] [CoDingSequence] U13636; AAB17019.1; -. [EMBL / GenBank / DDBJ] [CoDingSequence] |
| PIR | B23044; KIECGG. A13446; A13446. |
| EcoGene | EG10363; galk. |
| EcoCyc | EG10363; galk. |
| CMR | P06976; B0757. |
| HAMAP | MF_00246; -. 1. IPR000705; Galactokinase. IPR001174; Galkinase. IPR006204; GHMP_kinase. IPR006203; GHMPkinse_ATP. IPR006206; Mev_galkinase. Graphical view of domain structure. |
| Pfam | PF00288; GHMP_kinases; 1. PR00473; GALCTOKINASE. |
| PRINTS | PR00960; LMBPPROTEIN. PR00959; MEVGALKINASE. |
| TIGRFAMs | TIGR00131; gal_kin; 1. |
| PROSITE | PS00106; GALACTOKINASE; 1. PS00627; GHMP_KINASES_ATP; 1. |
| ProDom | [Domain structure / List of seq. sharing at least 1 domain]. |
| BLOCKS | P06976. |
| ProtoNet | P06976. |
| ProtoMap | P06976. |
| PRESAGE | P06976. |
| DIP | P06976. |
| ModBase | P06976. |
| SWISS-2DPAGE | Get region on 2D PAGE. |
| Keywords | Transferase; Kinase; Galactose metabolism; ATP-binding; Complete proteome. |

Features



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| Key | From | To | Length | Description |
|----------|------|-----|--------|-----------------|
| INIT_MET | 0 | 0 | | |
| NP_BIND | 121 | 131 | 11 | ATP (POTENTIAL) |

Sequence information

Length: 381 AA Molecular weight: 41311 Da CRC64: E4902DF7747288BA [This is a checksum on the sequence]

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| SLKEKTQSLF | ANAFGYPATH | TIQAEGRVNL | IGEHTDYNDG | FVLPCAIDYQ | TVISCAPRDD |
| 70 | 80 | 90 | 100 | 110 | 120 |
| RKVRVMAADY | ENQLDEFSLD | APIVAHENYQ | WANYVRGVVK | HLQLRNNSFG | GVDMVISGNV |
| 130 | 140 | 150 | 160 | 170 | 180 |
| PQGAGLSSSA | SLEVAVGTVL | QQLYHLPLDG | AQIALNGQEA | ENQFVGNCNG | IMDQLISALG |
| 190 | 200 | 210 | 220 | 230 | 240 |
| KKDHALLIDC | RSLGTKAVSM | PKGVAVVIIN | SNFKRTLVS | EYNTREQCE | TGARFFQQPA |
| 250 | 260 | 270 | 280 | 290 | 300 |
| LRDVTIEEFN | AVAHEDFIV | AKRVRHILTE | NARTVEAASA | LEQGDLMKRM | ELMAESHASM |
| 310 | 320 | 330 | 340 | 350 | 360 |
| RDDFEITVPQ | IDTLVEIVKA | VIGDKGGVRM | TGGGFGGCIV | ALIFEELVEA | VQQAQAEQYE |
| 370 | 380 | | | | |
| AKTGIKETFY | VCKPSQGAGQ | C | | | |

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| | |
|---|--|
| Official Name | |
| UDP-glucose 4-epimerase. | |
| Alternative Name(s) | |
| UDP-galactose 4-epimerase. Galactowaldenase. Uridine diphosphate galactose 4-epimerase. Uridine diphospho-galactose 4-epimerase. | |
| Reaction catalysed | |
| UDP-glucose <-> UDP-galactose | |
| Cofactor(s) | |
| NAD. | |
| Comments | |
| <ul style="list-style-type: none"> Also acts on UDP-2-deoxyglucose. | |
| Human Genetic Disease(s) | |
| Galactose epimerase deficiency | MIM:230350 |
| Cross-references | |
| Biochemical Pathways; map number(s) | B4, B5 |
| BRENDA | 5.1.3.2 |
| EMP/PUMA | 5.1.3.2 |
| WIT | 5.1.3.2 |
| KYOTO UNIVERSITY LIGAND CHEMICAL DATABASE | 5.1.3.2 |
| IUBMB Enzyme Nomenclature | 5.1.3.2 |
| MEDLINE | Find literature relating to 5.1.3.2 |
| Swiss-Prot | Q59083, EXOB_AZOB; Q59745, EXOB_RHIL; P26503, EXOB_RHME; Q42605, GAE1_ARATH; Q65780, GAE1_CYATE; Q43070, GAE1_PEA; Q9SN58, GAE2_ARATH; Q65781, GAE2_CYATE; Q9T0A7, GAE3_ARATH; Q9KDV3, GALE_BACHD; P55180, GALE_BACSU; P33119, GALE_CORDI; Q45291, GALE_CORGL; Q9W0F5, GALE_DROME; P09147, GALE_ECOLI; P35673, GALE_ERWAM; P24325, GALE_HAEIN; Q14376, GALE_HUMAN; P45602, GALE_KLEFN; Q84903, GALE_LACCA; Q57664, GALE_METJA; P47364, GALE_MYCGE; P75517, GALE_MYCPN; Q05026, GALE_NEIGO; P56997, GALE_NEIMA; P56985, GALE_NEIMB; P56986, GALE_NEIMC; Q59678, GALE_PASHA; Q9CNY5, GALE_PASMU; P18645, GALE_RAT; Q56093, GALE_SALTI; P22715, GALE_SALTY; P13226, GALE_STRLI; P96995, GALE_STRMU; P21977, GALE_STRTR; Q56623, GALE_VINCH; Q57301, GALE_YEREN; Q9F7D4, GALE_YERPE; P56600, GALE_CANMA; P09609, GALE_KLULA; P40801, GALE_PACTA; Q9HDU3, GALE_SCHPO; P04397, GALE_YEAST; |

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| Hosted by NCSC US Mirror sites: Canada China Korea Switzerland Taiwan | | | | |
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General information about the entry

Entry name **GALE_ECOLI**
Primary accession number **P09147**
Secondary accession numbers **None**
Entered in Swiss-Prot in **Release 10, March 1989**
Sequence was last modified in **Release 10, March 1989**
Annotations were last modified in **Release 41, February 2003**
Name and origin of the protein
Protein name **UDP-glucose 4-epimerase**
Synonyms **EC 5.1.3.2
Galactowaldenase
UDP-galactose 4-epimerase**
Gene name **GALE or GALD or B0759**
From **Escherichia coli (TaxID: 562)**
Taxonomy **Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales; Enterobacteriaceae; Escherichia**

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MEDLINE=87040735; PubMed=3022232; [NCBI, ExPASy, EBI, Israel, Japan]
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"Nucleotide sequences of the gal E gene and the gal T gene of E. coli.";
Nucleic Acids Res. 14:7705-7711(1986).
- [2] REVISIONS.
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Submitted (APR-1988) to the EMBL/GenBank/DBJ databases.
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STRAIN=K12 / MG1655;
MEDLINE=97426617; PubMed=9278503; [NCBI, ExPASy, EBI, Israel, Japan]
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V., Riley M., Collado-Vides J., Glasner L.D., Rode C.K., Mayhew G.F., Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J., Mau B., Shao Y.;
"The complete genome sequence of Escherichia coli K-12.";
Science 277:1453-1474(1997).
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- [5] SEQUENCE OF 1-31 FROM NUCLEIC ACID.
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"Molecular analysis of the molybdate uptake operon, modABCD, of Escherichia coli and modR, a regulatory gene.";
Microbiol. Res. 150:347-361(1995).
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MEDLINE=83183658; PubMed=6301942; [NCBI, ExPASy, EBI, Israel, Japan]
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"The molecular structure of UDP-galactose 4-epimerase from Escherichia coli determined at 2.5-A resolution.";
Proteins 12:372-381(1992).
- [8] X-RAY CRYSTALLOGRAPHY (1.8 ANGSTROMS).
MEDLINE=96180680; PubMed=8611559; [NCBI, ExPASy, EBI, Israel, Japan]
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"Crystal structures of the oxidized and reduced forms of UDP-galactose 4-epimerase isolated from Escherichia coli.";
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MEDLINE=97084800; PubMed=8931134; [NCBI, ExPASy, EBI, Israel, Japan]
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Protein Sci. 5:2149-2161(1996).
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MEDLINE=97317070; PubMed=9174344; [NCBI, ExPASy, EBI, Israel, Japan]
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- [11] X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS) OF SER-124 MUTANTS.
MEDLINE=97419132; PubMed=9271499; [NCBI, ExPASy, EBI, Israel, Japan]
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"Molecular structures of the S124A, S124T, and S124V site-directed mutants of UDP-galactose 4-epimerase from Escherichia coli.";
Biochemistry 36:10685-10695(1997).
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MEDLINE=98376428; PubMed=9708982; [NCBI, ExPASy, EBI, Israel, Japan]
Thoden J.B., Holden H.M.;
"Dramatic differences in the binding of UDP-galactose and UDP-glucose to UDP-galactose 4-epimerase from Escherichia coli.";
Biochemistry 37:11469-11477(1998).

Comments

- **CATALYTIC ACTIVITY:** UDP-glucose = UDP-galactose.
- **COFACTOR:** NAD.
- **PATHWAY:** Galactose metabolism; third step.
- **SUBUNIT:** Homodimer.
- **SIMILARITY:** BELONGS TO THE SUGAR EPIMERASE FAMILY.

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Cross-references

| | |
|------|---|
| EMBL | X06226; CAA29573.1; -. [EMBL / GenBank / DDBJ] [CoDingSequence] |
| | AE000178; AAC73846.1; -. [EMBL / GenBank / DDBJ] [CoDingSequence] |
| | D90714; BAA35421.1; -. [EMBL / GenBank / DDBJ] [CoDingSequence] |
| | U07867; AAB06890.1; -. [EMBL / GenBank / DDBJ] [CoDingSequence] |
| | J01613; AAA87978.1; -. [EMBL / GenBank / DDBJ] [CoDingSequence] |
| PIR | S02089; XUECUG. |
| | 2UDP; 18-MAR-98. [ExPASy / RCSB] |
| | 1NAH; 23-DEC-96. [ExPASy / RCSB] |
| | 1NAI; 23-DEC-96. [ExPASy / RCSB] |
| | 1XEL; 12-FEB-97. [ExPASy / RCSB] |
| PDB | 1UDA; 14-JAN-98. [ExPASy / RCSB] |
| | 1UDB; 14-JAN-98. [ExPASy / RCSB] |
| | 1UDC; 14-JAN-98. [ExPASy / RCSB] |
| | 1KVQ; 17-JUN-98. [ExPASy / RCSB] |
| | 1KVR; 18-MAR-98. [ExPASy / RCSB] |
| | 1KVS; 18-MAR-98. [ExPASy / RCSB] |
| | 1KVT; 18-MAR-98. [ExPASy / RCSB] |
| | 1KVU; 18-MAR-98. [ExPASy / RCSB] |
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1A9Y; 25-NOV-98. [ExPASy / RCSB]
 1A9Z; 25-NOV-98. [ExPASy / RCSB]
[Detailed list of linked structures.](#)

EcoGene [EG10362; galE.](#)

EcoCyc [EG10362; galE.](#)

CMR [P09147; B0759.](#)

InterPro [IPR001509; Epimerase_Dh.](#)

[IPR003886; GalE.](#)

[Graphical view of domain structure.](#)

Pfam [PF01370; Epimerase; 1.](#)

TIGRFAMs [TIGR01179; galE; 1.](#)

ProDom [\[Domain structure / List of seq. sharing at least 1 domain\].](#)

BLOCKS [P09147.](#)

ProtoNet [P09147.](#)

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PRESAGE [P09147.](#)

DIP [P09147.](#)

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Keywords

Isomerase; NAD; Galactose metabolism; 3D-structure; Complete proteome.

Features



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| Key | From | To | Length | Description |
|---------|------|-----|--------|------------------|
| NP_BIND | 2 | 33 | 32 | NAD (POTENTIAL). |
| STRAND | 2 | 6 | 5 | |
| TURN | 7 | 9 | 3 | |
| HELIX | 11 | 22 | 12 | |
| TURN | 23 | 24 | 2 | |
| STRAND | 26 | 31 | 6 | |
| TURN | 38 | 39 | 2 | |
| HELIX | 40 | 48 | 9 | |
| TURN | 49 | 49 | 1 | |
| STRAND | 53 | 56 | 4 | |
| TURN | 59 | 60 | 2 | |
| HELIX | 62 | 71 | 10 | |
| TURN | 72 | 73 | 2 | |
| STRAND | 76 | 79 | 4 | |
| HELIX | 86 | 91 | 6 | |
| HELIX | 93 | 114 | 22 | |
| TURN | 115 | 115 | 1 | |
| STRAND | 118 | 124 | 7 | |
| HELIX | 125 | 128 | 4 | |
| STRAND | 136 | 136 | 1 | |
| TURN | 138 | 139 | 2 | |
| HELIX | 148 | 166 | 19 | |
| TURN | 168 | 169 | 2 | |
| STRAND | 171 | 177 | 7 | |
| STRAND | 179 | 181 | 3 | |
| TURN | 185 | 186 | 2 | |
| HELIX | 200 | 208 | 9 | |
| TURN | 209 | 210 | 2 | |
| STRAND | 215 | 218 | 4 | |
| STRAND | 230 | 231 | 2 | |
| STRAND | 233 | 235 | 3 | |
| HELIX | 236 | 250 | 15 | |

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TURN      251  252    2
STRAND     255  261    7
STRAND     267  268    2
HELIX      269  280   12
TURN       281  281    1
STRAND     286  289    4
TURN       293  294    2
STRAND     298  298    1
STRAND     301  301    1
HELIX      304  310    7
HELIX      318  331   14
TURN       333  334    2

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Sequence information

Length: 338 AA Molecular weight: 37265 Da CRC64: 5CA8B4F7903F7792 [This is a checksum on the sequence]

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      |      |      |      |      |      |
MRVLVTGGSG YIGSHTCVQL LONGHDVIL DNLCSKRSV LPVIERLGK HPTFVEGDIR
      70      80      90     100     110     120
      |      |      |      |      |      |
NEALMTEILH DHAIDTVIHF AGLKAVGESV OKPLEYYDNN VNGTLRLISA MRAANVKNEI
     130     140     150     160     170     180
      |      |      |      |      |      |
FSSSATVYGD QPKIPYVESF PTGTRQSPYG KSKLMVEQIL TDLQKAQPDW SIALRLYFNP
     190     200     210     220     230     240
      |      |      |      |      |      |
VGAHPSGDMG EDPQGIPNNL MPYIAQVAVG ARSLAIFGN DYPTEDGTGV RDIYHVMDLA
     250     260     270     280     290     300
      |      |      |      |      |      |
DGHVVAMEKL ANKPGVHIYN LGAGVGNVSL DVVNAFSKAC GKPVNYHEAP RREGDLPAYW
     310     320     330
      |      |      |
ADASKADREL NWRVTRILDE MAQDTWHWQS RHPOGYPD

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[PeptideMass](#), [PeptideCutter](#), [Dotlet \(Java\)](#)[ScanProsite](#), [MotifScan](#)Search the [SWISS-MODEL Repository](#)[ExPASy Home page](#)[Site Map](#)[Search ExPASy](#)[Contact us](#)[Swiss-Prot](#)

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General information about the entry

Entry name **GAL7_ECOLI**
Primary accession number **P09148**
Secondary accession number **P78270**
Entered in Swiss-Prot in **Release 10, March 1989**
Sequence was last modified in **Release 35, November 1997**
Annotations were last modified in **Release 42, September 2003**
Name and origin of the protein
Protein name **Galactose-1-phosphate uridylyltransferase**
Synonyms **EC 2.7.7.12**
Gal-1-P uridylyltransferase
UDP-glucose-hexose-1-phosphate uridylyltransferase
Gene name **GALT or GALB or B0758**
From **[Escherichia coli](#) [TaxID: 562]**
Taxonomy **[Bacteria](#); [Proteobacteria](#); [Gammaproteobacteria](#); [Enterobacteriales](#);
[Enterobacteriaceae](#); [Escherichia](#).**

References

- [1] SEQUENCE FROM NUCLEIC ACID.
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Comments

- **CATALYTIC ACTIVITY:** UDP-glucose + alpha-D-galactose 1-phosphate = alpha-D-glucose 1-phosphate + UDP-galactose.
- **COFACTOR:** Binds 1 zinc and 1 iron ion per subunit.
- **PATHWAY:** Galactose metabolism; second step.
- **SUBUNIT:** Homodimer.
- **SIMILARITY:** Belongs to the galactose-1-phosphate uridylyltransferase family 1.

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Cross-references

| | |
|----------|---|
| EMBL | X06226; CAA29574.1; -. [EMBL / GenBank / DDBJ] [CoDingSequence] |
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| PIR | S00722; XNECUD. |
| | 1GUP; 12-NOV-97. [ExPASy / RCSB] |
| | 1GUQ; 12-NOV-97. [ExPASy / RCSB] |
| PDB | 1HXP; 08-NOV-96. [ExPASy / RCSB] |
| | 1HXQ; 22-OCT-97. [ExPASy / RCSB] |
| | Detailed list of linked structures. |
| EcoGene | EG10366; galT. |
| EcoCyc | EG10366; galT. |
| CMR | P09148; B0758. |
| InterPro | IPR001937; GalP_UDPtransf. |
| | IPR005851; GalP_Utransf_1. |
| | IPR005850; GalP_Utransf_C. |
| | IPR005849; GalP_Utransf_N. |
| | Graphical view of domain structure. |
| Pfam | PF02744; GalP_UDP_tr_C; 1. |
| | PF01087; GalP_UDP_transf; 1. |

ProDom PD005051; GalP_UDPtransfl; 1.
[Domain structure / List of seq. sharing at least 1 domain]
TIGRFAMs TIGR00209; galT_1; 1.
PROSITE PS00117; GAL_P_UDP_TRANSF_I; 1.
HOBACGEN [Family / Alignment / Tree]
BLOCKS P09148.
ProtoNet P09148.
ProtoMap P09148.
PRESAGE P09148.
DIP P09148.
ModBase P09148.
SWISS-2DPAGE Get region on 2D PAGE.

Keywords

Transferase; Zinc; Iron; Metal-binding; Nucleotidyltransferase; Galactose metabolism; 3D-structure;
Complete proteome.

Features



Feature table viewer

| Key | From | To | Length | Description |
|----------|------|-----|--------|------------------------|
| ACT_SITE | 166 | 166 | | NUCLEOPHILE. |
| METAL | 52 | 52 | | ZINC. |
| METAL | 55 | 55 | | ZINC. |
| METAL | 115 | 115 | | ZINC. |
| METAL | 164 | 164 | | ZINC. |
| METAL | 182 | 182 | | IRON. |
| METAL | 281 | 281 | | IRON. |
| METAL | 296 | 296 | | IRON. |
| METAL | 298 | 298 | | IRON. |
| CONFLICT | 29 | 31 | | AKR -> LS (IN REF. 1). |
| TURN | 6 | 8 | 3 | |
| STRAND | 11 | 15 | 5 | |
| TURN | 16 | 19 | 4 | |
| STRAND | 20 | 24 | 5 | |
| TURN | 26 | 27 | 2 | |
| HELIX | 28 | 30 | 3 | |
| TURN | 50 | 51 | 2 | |
| TURN | 53 | 54 | 2 | |
| TURN | 56 | 57 | 2 | |
| STRAND | 59 | 59 | 1 | |
| TURN | 61 | 62 | 2 | |
| STRAND | 65 | 65 | 1 | |
| STRAND | 73 | 76 | 4 | |
| TURN | 78 | 79 | 2 | |
| TURN | 84 | 85 | 2 | |
| STRAND | 99 | 101 | 3 | |
| STRAND | 104 | 110 | 7 | |
| TURN | 115 | 116 | 2 | |
| HELIX | 119 | 121 | 3 | |

| | | | |
|--------|-----|-----|----|
| HELIX | 124 | 144 | 21 |
| STRAND | 147 | 154 | 8 |
| HELIX | 156 | 158 | 3 |
| TURN | 159 | 159 | 1 |
| STRAND | 166 | 172 | 7 |
| HELIX | 177 | 193 | 17 |
| HELIX | 197 | 208 | 12 |
| TURN | 210 | 211 | 2 |
| STRAND | 212 | 215 | 4 |
| STRAND | 219 | 222 | 4 |
| TURN | 225 | 226 | 2 |
| TURN | 230 | 231 | 2 |
| STRAND | 233 | 237 | 5 |
| HELIX | 244 | 246 | 3 |
| HELIX | 249 | 270 | 22 |
| TURN | 271 | 271 | 1 |
| STRAND | 276 | 281 | 6 |
| TURN | 291 | 292 | 2 |
| STRAND | 296 | 300 | 5 |
| STRAND | 303 | 306 | 4 |
| TURN | 307 | 308 | 2 |
| STRAND | 309 | 310 | 2 |
| HELIX | 315 | 319 | 5 |
| TURN | 320 | 320 | 1 |
| STRAND | 323 | 324 | 2 |
| HELIX | 328 | 336 | 9 |
| TURN | 337 | 337 | 1 |
| HELIX | 343 | 346 | 4 |

Sequence information

Length: 348 AA Molecular weight: 39645 Da CRC64: 3D55D2CB38D8C9A2 [This is a checksum on the sequence]

| | | | | | |
|-------------|------------|------------|------------|------------|------------|
| 10 | 20 | 30 | 40 | 50 | 60 |
| MTQFNFPVDHP | HRRYNPLTGQ | WILVSPHRAK | RPWQGAQETP | AKQVLPADHP | DCFLCAGNVR |
| 70 | 80 | 90 | 100 | 110 | 120 |
| VTEGDKNPDIY | GTIVFTNDEA | ALMSDTFDAP | ESHDPIMRCQ | SARGTSRVIC | FSPDHSKTLF |
| 130 | 140 | 150 | 160 | 170 | 180 |
| ELSVAAALTEI | VKTWQEQTAE | LGKTYPWVQV | FENKGAAMGC | SNPHPHGQIW | ANSFLPNEAE |
| 190 | 200 | 210 | 220 | 230 | 240 |
| REDRLQKEYF | AEQKSPMLVD | YVQRELADGS | RTVVETEHWL | AVVPYWAAMP | FETLLLPKAE |
| 250 | 260 | 270 | 280 | 290 | 300 |
| VLRTDLTDA | QRSDLALALK | KLTSRYDNLF | QCSFPYSMGW | HGAPFNGEEN | QHWQLHAHFY |
| 310 | 320 | 330 | 340 | | |
| DPLLRSATVR | KFMVGYEMLA | ETQRDLTAEQ | AAERLRRAVD | IHFRESGV | |

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[pI/Mw](#), [PeptideMass](#), [PeptideCutter](#), [Dotlet \(Java\)](#)



[ScanProsite](#), [MotifScan](#)



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